

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2000, 17:37:18 ; Search time 904.17 Seconds
(without alignments)
-6360.431 Million cell updates/sec

Title: US-09-126-945-1
Perfect score: 1894
Sequence: 1 gctgactctccctccagcagc.....ataagatctactagagactg 1894
Scoring table: IDENTITY_NUC
Searched: 821193 seqs, -1518192014 residues
Database: GenEmbl:*
Word size: 0
Number of hits that pass the threshold: 1642386

1: gb_dal:*
2: gb_dal:*
3: gb_dal:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
7: gb_ov:*
8: gb_ov:*
9: gb_ov:*
10: gb_ov:*
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13: gb_ov:*
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18: gb_ov:*
19: gb_ov:*
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45: gb_ov:*
46: gb_ov:*
47: gb_ov:*
48: gb_ov:*
49: gb_ov:*

50: gb_p13:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1894	100.0	1894	40	AF071538	AF071538 Homo sapi
2	751.2	39.7	1704	12	AB019436	AB019436 Mus muscu
3	150.8	8.0	362	35	DRODER54A	M88474 Drosophila
4	150.8	8.0	139371	41	AC008253	AC008253 Drosophila
5	150.8	8.0	38178	43	AC015374	AC015374 Drosophila
6	147.6	7.8	1832	35	AF106964	AF106964 Strongylo
7	147.6	7.8	137899	43	AC007818	AC007818 Drosophila
8	134.2	7.1	121935	33	AC008217	AC008217 Drosophila
9	99.2	5.2	6479	34	DROE74A	M37082 Drosophila
10	99.2	5.2	5315	34	DROE74B	M37083 Drosophila
11	97.6	5.2	4800	34	DM74E	X15087 Drosophila
12	97.6	5.2	115815	42	AC009371	AC009371 Drosophila
13	86.4	4.6	2635	9	AB016193	AB016193 Homo sapi
14	86.4	4.6	2266	9	HUMELK1A	M25269 Homo sapien
15	84.8	4.5	848	4	AF075706	AF075706 Gallus ga
16	84.4	4.5	742	40	AF000672	AF000672 Homo sapi
17	84	4.4	1436	4	DRE249590	AJ249590 Dario rer
18	83.6	4.4	2286	12	MMELK1G	X87257 M.musculus
19	83.6	4.4	660	12	MMELK1P	Z36939 M.musculus
20	83.4	4.4	1403	9	HSDNAFEV3	Y08976 H.sapiens F
21	83.4	4.4	1901	9	HSRNAFEV	Y08976 H.sapiens m
22	82.8	4.4	2508	4	AF075708	AF075708 Gallus ga
23	82.4	4.4	4200	4	DRU84615	U84615 Dario rerio
24	81.4	4.3	1245	4	AF177538	AF177538 Dario rer
25	81.4	4.3	3386	12	AF016714	AF016714 Mus muscu
26	79.8	4.2	1447	40	AF147782	AF147782 Homo sapi
27	78.4	4.1	2667	5	AR026645	AR026645 Sequence
28	78.4	4.1	2667	5	HSU15655	U15655 Human ets d
29	78.4	4.1	4190	10	HSU32845	U32845 Human myelo
30	78.4	4.1	4007	11	AF000670	AF000670 Homo sapi
31	78.2	4.1	2529	10	AF017307	AF017307 Homo sapi
32	78.2	4.1	1907	10	HSU6894	U6894 Human epilch
33	78.2	4.1	1915	10	HSU73843	U73843 Homo sapien
34	78.2	4.1	1846	10	HSU73844	U73844 Homo sapien
35	78.2	4.1	1942	11	HSU97156	U97156 Homo sapien
36	78.2	4.1	2642	40	HSU7575	AF095890 Homo sapi
37	78	4.1	473	5	E06024	E06024 CDNA encodi
38	78	4.1	2073	5	E06025	E06025 CDNA encodi
39	78	4.1	100000	9	AP000021	AP000021 Homo sapi
40	78	4.1	2064	9	HUMELAF	D12765 Human mRNA
41	78	4.1	100000	10	AP000163	AP000163 Homo sapi
42	78	4.1	2333	10	HSU18018	U18018 Human E1A e
43	78	4.1	2107	40	HSU35622	U35622 Homo sapien
44	77.4	4.1	1910	12	AF016294	AF016294 Mus muscu
45	77.2	4.1	3126	9	HUMERG11	M21535 Human erg p

ALIGNMENTS

RESULT 1
AF071538
LOCUS AF071538 1894 bp mRNA
DEFINITION Homo sapiens Ets transcription factor, PDEF (PDEF) mRNA, complete cds.
ACCESSION AF071538
VERSION AF071538.1 GI:4007417
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

FEATURES	source
ORGANISM	Mus musculus
REFERENCE	AB019436
AUTHORS	AB019436
JOURNAL	Prostate specific transcription factor ets, mpae.
REFERENCE	Mus musculus (strain:C57BL/6) Adult male Colon Epithelial CDNA to mRNA.
AUTHORS	Mus musculus
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 1704)
JOURNAL	Nozaki, M.
REFERENCE	Prostate specific ets
AUTHORS	Published Only in Database (1999) In press
JOURNAL	2 (bases 1 to 1704)
REFERENCE	Nozaki, M.
TITLE	Direct Submission
JOURNAL	Submitted (02-NOV-1998) to the DBJ/EMBL/GenBank databases. Masami Nozaki, Osaka University, Institute for Microbial Diseases, 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan
REFERENCE	(E-mail:mozaki@ibiken.osaka-u.ac.jp, Tel:81-6-879-8338, Fax:81-6-879-8339)
FEATURES	Location/Qualifiers
source	1..1704
organism	"Mus musculus"
strain	"C57BL/6"
db_xref	"taxon:10090"
cell_type	"Epithelial"
dev_stage	"Adult"
sex	"male"
tissue_type	"Colon"
362..1339	
gene	"mpae"
362..1339	
gene	"mpae"
codon_start	1
product	"Prostate specific transcription factor ets"
protein_id	"BA073329.1"
db_xref	"GI:4760537"
translation	"MGSASPGLSNVPSCCLLPDVAPRTGTERKASGAMPEKQNS PSPAPTEOGISAPYLSIFNNYPPDSSNVAVPERAKEDPEPBOCPYVDSAGSS TLDESLSEQSNVVEYLKDIETACKLINTADGDSPEVORWILMTGHORLPPE AGKAEQVIGKELCAMESEORRORAPLGGDVLHMLDITKSAAMKEKTSGLTYCA STSEGWTDSEVSDSCOPILHLMQFLKEILLKHSYGRFRLMLNKEGIRIDSDAQ VARLSEGWKRNPNAMYDKLTSRSIRQYKKGIIIRPDIQRVLYOFVHEV"

[illegible]

QY 998 tgcgcccctgggtggatgtgtcgtacacgcccacattgacatctggaagtcagcgccctgg 1057
 Db 914 GCACCTTGGGTGGGATGATGACTCATGCGCCACTGGGACATCTGGAATGACGCGCTGG 973
 QY 1058 atgaaagagagagacttaccctggggcgattactactgtgtcctgacacagtgaaagagc 1117
 Db 974 ATGAAG 1033
 QY 1118 tggacacag 1177
 Db 1034 TGGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1093
 QY 1178 ctcaagagatgtctactcaagagagagagagagagagagagagagagagagagagag 1237
 Db 1094 CTGAAGAAAGT 1153
 QY 1238 gagaag 1297
 Db 1154 GAGAAAGGCAATCTTCAAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1213
 QY 1298 aagaacgctccgcatgaaactagacagagagagagagagagagagagagagagagag 1357
 Db 1214 AAGAAACGGGCGAG 1273
 QY 1358 aaggagatctccggaag 1417
 Db 1274 AAGGGCATCTATCTGTAACCCGACATCTCTACAGCGCTGTCTACAAATTTGTGATCA 1333
 QY 1418 atctgagtgcc---tggccagagagagagagagagagagagagagagagagagagag 1473
 Db 1334 GTCTGAG 1393
 QY 1474 gccctgcc 1481
 Db 1394 GCCTGCTC 1401

RESULT 3
 DRODETS4A 362 bp DNA INV 28-SEP-1999
 LOCUS Drosophila melanogaster chromosome 3 D-ets-4 DNA binding domain
 DEFINITION protein gene, partial cds.
 ACCESSION M88474
 VERSION M88474.1 GI:157195
 KEYWORDS
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
 1 (bases 1 to 362)
 Chen, T., Buntling, M., Karim, F.D. and Thummel, C.S.
 Isolation and characterization of five Drosophila genes that encode
 an ets-related DNA binding domain
 Dev. Biol. 151, 176-191 (1992)
 92249640

FEATURES
 MEDLINE
 JOURNAL
 TITLE
 AUTHORS
 REFERENCE
 SOURCE
 location/Qualifiers
 1..362
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /chromosome="3"
 /map="3R: 98B"
 <1..>345
 /product="D-ets-4 DNA binding domain protein"
 1..362
 /gene="Ets98B"
 /note="Ets at 98B"
 /allele=""
 /db_xref="FlyBase:Fggn0005659"
 <1..345
 /codon_start=1
 /product="D-ets-4 DNA binding domain protein"

CDS

BASE COUNT 90 a 99 c 113 g 60 t
 ORIGIN

Query Match 8.0%; Score 150.8; DB 35; Length 362;
 Best Local Similarity 72.9%; Pred. No. 1.5e-17;
 Matches 194; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1157 cccatccacctgtggcagattctcctaagagatgtactcaagagagagagagagagagag 1216
 Db 73 CACATCCACCTGTGGCAGTTCCTCAAGAGAGGTGTGGCTTCCAGGTGAACGGCACA 132
 QY 1217 ttcattagtggtctcaagaagagagagagagagagagagagagagagagagagagag 1276
 Db 133 GCCATCCGCGTGTGATGACCGAAGCAAGGCGCATCTTCAAGATGAGAGAGTGGTAGG 192
 QY 1277 gccggctgtgtgggcatccggaagagagagagagagagagagagagagagagagag 1336
 Db 193 GCCAAGCTGTGGGCTCGCGCAAGAACCGGCGGATGAGACTATGATTAAGTTTCCCG 252
 QY 1337 tccatccgcatgattacaagaagagagagagagagagagagagagagagagagagag 1396
 Db 253 TCCATCAG 312
 QY 1397 gtctacagatctgtgtcagagagagagagagagagagagagagagagagagagag 1422
 Db 313 GTCATCAGATCTGTGCGATCCTTACAG 338

RESULT 4
 AC008253/c 139371 bp DNA HTG 24-SEP-1999
 LOCUS Drosophila melanogaster chromosome 3 clone BACR48A16 (D55b) RPT-98
 DEFINITION 48.A.16 map 98B1-98B2 strain y; cn bw sp, *** SEQUENCING IN
 PROGRESS ***; 82 unoriented pieces.
 ACCESSION AC008253 GI:5922044
 VERSION AC008253.6
 KEYWORDS HTG; HTGS-PHASE1.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
 1 (bases 1 to 139371)
 Ceiniker, S.E., Agdayani, A., Arcana, T.T., Baxter, E., Blazek, R.G.,
 Butenheff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
 Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
 Hoskins, R.A., Houston, K.A., Hummels, S.R., Katta, K., Kearney, L.,
 Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,
 Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacileo, J.M., Park, S.,
 Pfeiffer, B., Poon, L., Sequelstra, A., Sethi, H., Shtr, E.,
 Sylvestras, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and
 Rubin, G.M.
 Sequencing of Drosophila melanogaster
 unpublished

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 2 (bases 1 to 139371)
 Ceiniker, S.E., Agdayani, A., Arcana, T.T., Baxter, E., Blazek, R.G.,
 Butenheff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
 Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
 Hoskins, R.A., Houston, K.A., Hummels, S.R., Katta, K., Kearney, L.,
 Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,
 Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacileo, J.M., Park, S.,
 Pfeiffer, B., Poon, L., Sequelstra, A., Sethi, H., Shtr, E.,
 Sylvestras, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and
 Rubin, G.M.
 Direct Submission
 Submitted (30-Jul-1999) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA

COMMENT

On Sep 24, 1999 this sequence version replaced g1:5902266.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive Web site (<http://www.fruitfly.org/sequence/>) or send email
 to bdg@fruitfly.berkeley.edu. All contigs in this submission meet
 the following cutoffs: length >= 200 bases.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 82 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 572: contig of 572 bp in length
 * 573 652: gap of unknown length
 * 653 1162: contig of 510 bp in length
 * 1163 1242: gap of unknown length
 * 1243 1918: contig of 676 bp in length
 * 1919 1998: gap of unknown length
 * 1999 2663: contig of 665 bp in length
 * 2664 2743: gap of unknown length
 * 2744 3404: contig of 661 bp in length
 * 3405 3484: gap of unknown length
 * 3485 3914: contig of 430 bp in length
 * 3915 3994: gap of unknown length
 * 3995 4657: contig of 663 bp in length
 * 4658 4737: gap of unknown length
 * 4738 5423: contig of 686 bp in length
 * 5424 5503: gap of unknown length
 * 5504 6335: contig of 832 bp in length
 * 6336 6415: gap of unknown length
 * 6416 7396: contig of 981 bp in length
 * 7397 7476: gap of unknown length
 * 7477 8037: contig of 561 bp in length
 * 8038 8117: gap of unknown length
 * 8118 9339: contig of 1222 bp in length
 * 9340 9419: gap of unknown length
 * 9420 10121: contig of 702 bp in length
 * 10122 10201: gap of unknown length
 * 10202 10761: contig of 560 bp in length
 * 10762 10841: gap of unknown length
 * 10842 11485: contig of 644 bp in length
 * 11486 11565: gap of unknown length
 * 11566 12176: contig of 611 bp in length
 * 12177 12256: gap of unknown length
 * 12257 13142: contig of 886 bp in length
 * 13143 13222: gap of unknown length
 * 13223 13874: contig of 652 bp in length
 * 13875 13954: gap of unknown length
 * 13955 15117: contig of 1163 bp in length
 * 15118 15197: gap of unknown length
 * 15198 16153: contig of 956 bp in length
 * 16154 16233: gap of unknown length
 * 16234 16976: contig of 743 bp in length
 * 16977 17056: gap of unknown length
 * 17057 18209: contig of 1153 bp in length
 * 18210 18289: gap of unknown length
 * 18290 19765: contig of 1476 bp in length
 * 19766 19845: gap of unknown length
 * 19846 21223: contig of 1378 bp in length
 * 21224 21303: gap of unknown length
 * 21304 22618: contig of 1315 bp in length
 * 22619 22698: gap of unknown length
 * 22699 24057: contig of 1359 bp in length
 * 24058 24137: gap of unknown length
 * 24138 24963: contig of 826 bp in length
 * 24964 25043: gap of unknown length
 * 25044 26302: contig of 1259 bp in length
 * 26303 26382: gap of unknown length
 * 26383 27193: contig of 811 bp in length
 * 27194 27273: gap of unknown length
 * 27274 28205: contig of 932 bp in length

28206 28285: gap of unknown length
 * 28286 29927: contig of 1642 bp in length
 * 29928 30007: gap of unknown length
 * 30008 31006: contig of 999 bp in length
 * 31007 31086: gap of unknown length
 * 31087 31995: contig of 909 bp in length
 * 31996 32075: gap of unknown length
 * 32076 33297: contig of 1222 bp in length
 * 33298 33377: gap of unknown length
 * 33378 35041: contig of 1664 bp in length
 * 35042 35121: gap of unknown length
 * 35122 36763: contig of 1642 bp in length
 * 36764 36843: gap of unknown length
 * 36844 37498: contig of 655 bp in length
 * 37499 37578: gap of unknown length
 * 37579 38912: contig of 1334 bp in length
 * 38913 38992: gap of unknown length
 * 38993 40750: contig of 1758 bp in length
 * 40751 40830: gap of unknown length
 * 40831 42653: contig of 1823 bp in length
 * 42654 42733: gap of unknown length
 * 42734 44356: contig of 1623 bp in length
 * 44357 44436: gap of unknown length
 * 44437 46335: contig of 1899 bp in length
 * 46336 46415: gap of unknown length
 * 46416 47879: contig of 1464 bp in length
 * 47880 47959: gap of unknown length
 * 47960 49760: contig of 1801 bp in length
 * 49761 49840: gap of unknown length
 * 49841 51596: contig of 1756 bp in length
 * 51597 51676: gap of unknown length
 * 51677 52715: contig of 1039 bp in length
 * 52716 52795: gap of unknown length
 * 52796 54355: contig of 1560 bp in length
 * 54356 54435: gap of unknown length
 * 54436 55545: contig of 1110 bp in length
 * 55546 55625: gap of unknown length
 * 55626 57376: contig of 1751 bp in length
 * 57377 57456: gap of unknown length
 * 57457 60745: contig of 3289 bp in length
 * 60746 60825: gap of unknown length
 * 60826 62405: contig of 1580 bp in length
 * 62406 62485: gap of unknown length
 * 62486 63859: contig of 1374 bp in length
 * 63860 63939: gap of unknown length
 * 63940 65968: contig of 2029 bp in length
 * 65969 66048: gap of unknown length
 * 66049 68286: contig of 2238 bp in length
 * 68287 68366: gap of unknown length
 * 68367 70709: contig of 2343 bp in length
 * 70710 70789: gap of unknown length
 * 70790 72901: contig of 2112 bp in length
 * 72902 72981: gap of unknown length
 * 72982 76175: contig of 3194 bp in length
 * 76176 76255: gap of unknown length
 * 76256 79093: contig of 2838 bp in length
 * 79094 79173: gap of unknown length
 * 79174 80841: contig of 1668 bp in length
 * 80842 80921: gap of unknown length
 * 80922 83209: contig of 2288 bp in length
 * 83210 83289: gap of unknown length
 * 83290 85034: contig of 1745 bp in length
 * 85035 85114: gap of unknown length
 * 85115 88635: contig of 3521 bp in length
 * 88636 88715: gap of unknown length
 * 88716 92350: contig of 3635 bp in length
 * 92351 92430: gap of unknown length
 * 92431 96637: contig of 4207 bp in length
 * 96638 96717: gap of unknown length
 * 96718 101119: contig of 4402 bp in length
 * 101120 101199: gap of unknown length
 * 101200 105863: contig of 4664 bp in length
 * 105864 105943: gap of unknown length

Query Match 7.8%; Score 147.6; DB 35; Length 1832;
 Best Local Similarity 73.3%; Pred. No. 3.8e-17;
 Matches 189; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1160 atccacatgagcagtcctcctcaagagctgtctacacagccacagctatgagcgcttc 1219
 Db 962 ATCCAGCTCTGGCAGTTCTTGAAGAGAGCTCCTCTCAGCCCAACTCTACACTACTG 1021
 Qy 1220 attagtgctcacaagaagagagagcattcttaaatgtgagactccagccggcgcc 1279
 Db 1022 ATCAGGTGATACAGAACACACAGATATCTTCAAGATCAGAGACTCTGCGAGGTCGCC 1081
 Qy 1280 cggctctggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1339
 Db 1082 AGACTTGGGGCTTGAAGAAAGAACAGCCCGCATGACATACAGCAAGCTCTCTGCTCC 1141
 Qy 1340 atccgacagatattacaagaagagcagcagcagcagcagcagcagcagcagcagcagc 1399
 Db 1142 ATCAGGAGTACTACCGCAAGGATCATGAAAGACAGCAGGTTTCGAGCAGCTCTGTC 1201
 Qy 1400 taccattcgtgcacccc 1417
 Db 1202 TACGAGTTTGTACCCCC 1219

RESULT / 7

AC007818/c 137899 bp DNA HTG 16-NOV-1999
 LOCUS Drosophila melanogaster chromosome 3 clone BACR02M05 (D788) RPCT-98
 DEFINITION 02.M.5 map 98B-98B strain Y; cn bw sp. *** SEQUENCING IN PROGRESS
 ** 81 unordered pieces.

AC007818 4 GI:6435861
 AC007818 HTG: HTG_PHASE1.
 SOURCE Fruit fly.
 ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Endopterygota; Diptera; Brachycera;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 137899)

AUTHORS Celiker,S.E., Agbayani,A., Arcalena,T.T., Baxter,E., Blazek,R.G.,
 Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
 Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
 Hinkle,A., Hoakins,R.A., Houston,K.A., Hummasti,S.R., Karra,K.,
 Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R.,
 Moshrefi,M., Nixon,K., Pacled,J.M., Park,S., Pfeiffer,B.,
 Richards,S., Sethi,H., Svitskas,R.R., Wan,K.H., Webster,D.,
 Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.
 Sequencing of Drosophila melanogaster
 unpublished

TITLE 2 (bases 1 to 137899)
 JOURNAL
 REFERENCE
 AUTHORS

TITLE Direct Submission
 JOURNAL Submitted (14-JUN-1999) Drosophila Genome Center, Lawrence Berkeley
 COMMENT Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Nov 16, 1999 this sequence version replaced gi:5670465.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive web site (<http://www.fruitfly.org/sequence/>) or send email
 to bdg@fruitfly.berkeley.edu. All contigs in this submission meet
 the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 81 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1023: contig of 1023 bp in length
 1024 1103: gap of unknown length
 1104 2410: contig of 1307 bp in length
 2411 2490: gap of unknown length
 2491 3408: contig of 918 bp in length
 3409 3489: gap of unknown length
 3489 4264: contig of 776 bp in length
 4265 4344: gap of unknown length
 4345 4976: contig of 632 bp in length
 4977 5057: gap of unknown length
 5057 5891: contig of 835 bp in length
 5892 5971: gap of unknown length
 5971 6910: contig of 939 bp in length
 6911 7680: gap of unknown length
 7681 7760: contig of 690 bp in length
 7761 8137: gap of unknown length
 8138 8217: contig of 377 bp in length
 8218 8883: gap of unknown length
 8884 8963: contig of 666 bp in length
 8964 9954: gap of unknown length
 9955 10034: contig of 991 bp in length
 10035 10722: gap of unknown length
 10723 10802: contig of 688 bp in length
 10803 11555: gap of unknown length
 11556 11635: contig of 753 bp in length
 11636 12241: gap of unknown length
 12242 12321: contig of 606 bp in length
 12322 13469: gap of unknown length
 13470 13549: contig of 118 bp in length
 13550 14845: gap of unknown length
 14846 14925: contig of 1296 bp in length
 14926 16090: gap of unknown length
 16091 16170: contig of 1165 bp in length
 16171 17409: gap of unknown length
 17410 17489: contig of 1239 bp in length
 17490 18567: gap of unknown length
 18568 18647: contig of 1078 bp in length
 18648 20255: gap of unknown length
 20256 20335: contig of 1608 bp in length
 20336 22111: gap of unknown length
 22112 22191: contig of 1776 bp in length
 22192 23746: gap of unknown length
 23747 23826: contig of 1555 bp in length
 23827 25242: gap of unknown length
 25243 25322: contig of 1416 bp in length
 25323 27339: gap of unknown length
 27340 27419: contig of 2017 bp in length
 27420 29015: gap of unknown length
 29016 31254: contig of 1596 bp in length
 31255 31334: gap of unknown length
 31335 32458: contig of 2159 bp in length
 32459 32538: gap of unknown length
 32539 34371: contig of 1124 bp in length
 34372 34451: gap of unknown length
 34452 36983: gap of unknown length
 36984 37063: contig of 1833 bp in length
 37064 38444: gap of unknown length
 38445 38524: contig of 1381 bp in length
 38525 40637: gap of unknown length
 40638 40717: contig of 2113 bp in length
 40718 42339: gap of unknown length
 42339 42419: contig of 1622 bp in length
 42420 44343: gap of unknown length
 44344 44424: contig of 1924 bp in length
 44425 46038: gap of unknown length
 46039 46118: contig of 1615 bp in length
 46119 46039: gap of unknown length

[illegible]

TITLE Sequencing of *Drosophila melanogaster*
JOURNAL
REFERENCE
AUTHORS 2 (bases 1 to 121935)
Celniker, S.E., Agbayan, A., Arcata, T.T., Baxter, E., Blazej, R.G.,
Buenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomocan, M.A., Mazda, P.,
Moshirei, A.R., Moshirei, M., Nixon, K., Patel, J.M., Park, S.,
Pfeiffer, B., Poon, L., Sequeira, A., Sechl, H., Solfr, E.,
Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
Rubin, G.M.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1999) *Drosophila* Genome Center, Lawrence Berkeley

COMMENT

Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Aug 2, 1999 this sequence version replaced g1.5649213.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (<http://www.fruitfly.org/sequence/>) or send email
to bede@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 94 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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847	925:	gap of unknown length
927	1629:	contig of 703 bp in length
1630	1709:	gap of unknown length
1710	2954:	contig of 1245 bp in length
2955	3034:	gap of unknown length
3035	4305:	contig of 1271 bp in length
4306	4385:	gap of unknown length
4386	5409:	contig of 1024 bp in length
5410	5489:	gap of unknown length
5490	6507:	contig of 1018 bp in length
6508	6587:	gap of unknown length
6588	7425:	contig of 838 bp in length
7426	7505:	gap of unknown length
7506	8262:	contig of 757 bp in length
8263	8342:	gap of unknown length
8343	9210:	contig of 868 bp in length
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9291	10030:	contig of 740 bp in length
10031	10110:	gap of unknown length
10111	10647:	contig of 537 bp in length
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10728	11695:	contig of 968 bp in length
11696	11775:	gap of unknown length
11776	12463:	contig of 688 bp in length
12464	12543:	gap of unknown length
12544	13186:	contig of 643 bp in length
13187	13266:	gap of unknown length
13267	14623:	contig of 1357 bp in length
14624	14703:	gap of unknown length
14704	15407:	contig of 704 bp in length
15408	15487:	gap of unknown length
15488	16114:	contig of 627 bp in length
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18152	18231:	gap of unknown length
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19327	19406:	gap of unknown length
19407	20721:	contig of 1315 bp in length
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20802	22114:	contig of 1313 bp in length
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22195	23387:	contig of 1193 bp in length
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24419	25754:	contig of 1336 bp in length
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25835	27378:	contig of 1544 bp in length
27379	27458:	gap of unknown length
27459	28093:	contig of 635 bp in length
28094	28173:	gap of unknown length
28174	29498:	contig of 1325 bp in length
29499	29578:	gap of unknown length
29579	30453:	contig of 875 bp in length
30454	30533:	gap of unknown length

30534	31577:	contig of 1044 bp in length
31578	31657:	gap of unknown length
31658	32852:	contig of 1195 bp in length
32853	32932:	gap of unknown length
32933	34455:	contig of 1523 bp in length
34456	34535:	gap of unknown length
34536	36322:	contig of 1787 bp in length
36323	36402:	gap of unknown length
36403	37400:	contig of 998 bp in length
37401	37480:	gap of unknown length
37481	39348:	contig of 1868 bp in length
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39429	40943:	contig of 1515 bp in length
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41024	41834:	contig of 811 bp in length
41835	41914:	gap of unknown length
41915	43233:	contig of 1319 bp in length
43234	43313:	gap of unknown length
43314	45758:	contig of 2445 bp in length
45759	45838:	gap of unknown length
45839	47770:	contig of 1932 bp in length
47771	47850:	gap of unknown length
47851	48194:	contig of 1344 bp in length
48195	48274:	gap of unknown length
49275	50726:	contig of 1452 bp in length
50727	50806:	gap of unknown length
50807	52379:	contig of 1573 bp in length
52380	52459:	gap of unknown length
52460	53703:	contig of 1244 bp in length
53704	53783:	gap of unknown length
53784	55620:	contig of 1837 bp in length
55621	55700:	gap of unknown length
55701	57561:	contig of 1861 bp in length
57562	57641:	gap of unknown length
57642	59011:	contig of 2260 bp in length
59012	59981:	gap of unknown length
59982	61047:	contig of 1066 bp in length
61048	61127:	gap of unknown length
61128	62765:	contig of 1638 bp in length
62766	62845:	gap of unknown length
62846	65301:	contig of 2456 bp in length
65302	65381:	gap of unknown length
65382	66683:	contig of 1302 bp in length
66684	66763:	gap of unknown length
66764	68942:	contig of 2179 bp in length
68943	69022:	gap of unknown length
69023	70711:	contig of 1689 bp in length
70712	70791:	gap of unknown length
70792	72773:	contig of 1982 bp in length
72774	72853:	gap of unknown length
72854	75671:	contig of 2818 bp in length
75672	75751:	gap of unknown length
75752	77673:	contig of 1924 bp in length
77674	77753:	gap of unknown length
77755	80249:	contig of 2494 bp in length
80250	80329:	gap of unknown length
80330	83371:	contig of 3042 bp in length
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83452	85544:	contig of 3093 bp in length
85545	86524:	gap of unknown length
86525	90786:	contig of 4162 bp in length
90787	90866:	gap of unknown length
90867	96542:	contig of 5676 bp in length
96543	96622:	gap of unknown length
96623	97226:	contig of 604 bp in length
97227	97306:	gap of unknown length
97307	98029:	contig of 723 bp in length
98030	98109:	gap of unknown length
98110	98868:	contig of 759 bp in length
98869	98948:	gap of unknown length
98949	99550:	contig of 602 bp in length
99551	99630:	gap of unknown length
99631	100459:	contig of 829 bp in length

* 100460 100539: gap of unknown length
 * 100540 101185: contig of 646 bp in length
 * 101186 101265: gap of unknown length
 * 101266 102112: contig of 847 bp in length
 * 102113 102192: gap of unknown length
 * 102193 102875: contig of 683 bp in length
 * 102876 102955: gap of unknown length
 * 102956 103709: contig of 754 bp in length
 * 103710 103789: gap of unknown length
 * 103790 104473: contig of 684 bp in length
 * 104474 104553: gap of unknown length
 * 104554 105266: contig of 713 bp in length
 * 105267 105346: gap of unknown length
 * 105347 106066: contig of 720 bp in length
 * 106067 106146: gap of unknown length
 * 106147 106779: contig of 633 bp in length
 * 106780 106859: gap of unknown length
 * 106860 107542: contig of 683 bp in length

Query Match 7.1%; Score 134.2; DB 33; Length 121935;
 Best Local Similarity 54.6%; Pred. No. 3.1e-15;
 Matches 172; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 1157 cccatccacctgtgagcttctcctcaaggagttgctactcaagcccccacagctatggcgc 1216
 DB 23155 CACATCCACTGTGGCAGTTCTCCAGAGAGCTGCTGCTCCGCCAGGTGAACGGCACA 23214
 QY 1217 ttcattagttgctcaacaaggagagctcttcaaaattgaggaactcagccagtg 1276
 DB 23215 GCCATCGGTGATCGATCGAGCAAGGCGCATCTTCAGATCGAAGACTCACTGAGGGTG 23274
 QY 1277 gccgagctgtggagcctcgcgaagacgcgtccgcagctgaactaagacagctgagccgc 1336
 DB 23275 GCCAGCTGTGGGCTCCGCGCAAGAACCGACCGCGCATGATGATGATGTTGTCGCCG 23334
 QY 1337 tccatccgcaglatatcaagaaggacatccgcgaagccagacatccagagcctc 1396
 DB 23335 TCATCAGCGACTACTACAGAGAAAGGAATCATGAGAAGACGAGACAGCTCACANNNNNN 23394
 QY 1397 gctaccagttcgtgcaccccatctgagtgcctgcgcagggcctgaaaccgcctcag 1456
 DB 23395 NNN 23454
 QY 1457 gggcctctctcctgc 1471
 DB 23455 NNNNNNNNNNNNGC 23469

RESULT 9
 DROE74A DROE74A 6479 bp mRNA INV 26-APR-1993
 LOCUS Drosophila melanogaster E74A protein.
 DEFINITION M37082.1 GI:157307
 ACCESSION
 VERSION
 KEYWORDS DNA-binding protein; E74A protein.
 SOURCE D.melanogaster (strain Canton S), cDNA to mRNA, and DNA.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 6479)
 AUTHORS Butts,K.C., Thummel,C.S., Jones,C.W., Karim,F.D. and Hogness,D.S.
 TITLE The Drosophila E74E early puff contains E74, a complex
 JOURNAL ecdysone-inducible gene that encodes two ets-related proteins
 MEDLINE Cell 61, 85-99 (1990)
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
 FEATURES by C.S.Thummel, 10-Sep-1990.
 source Location/Qualifiers
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 /strain="Canton S"
 /db_xref="taxon:7227"

gene

/map="3L 74EF"
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 /note="Ecdysone-induced protein 74EF"
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CDS

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polyA_signal

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 /db_xref="FlyBase:FBgn0000567"

BASE COUNT 1879 a 1641 c 1481 g 1478 t
 ORIGIN

Query Match 5.2%; Score 99.2; DB 34; Length 6479;
 Best Local Similarity 64.5%; Pred. No. 9.7e-09;
 Matches 165; Conservative 0; Mismatches 88; Indels 3; Gaps 1;

QY 1158 ccatccacctgtgagcttctcctcaaggagttgctactcaagcccccacagctatggcgc 1217
 DB 4572 CCACCTATCTGTGGAGTTCTCTCAAACTGCTCCAGAGTCCGAACTACTGCTCCCGTT 4631
 QY 1218 tccattagttgctcaacaaggagagctcttcaaaattgaggaactcagccagtg 1277
 DB 4632 TCATCAAGTGAAGAACCGGAGAGAGCGGCTCTTCAAGCTGGTCACTGAAAGCTGTGT 4691
 QY 1278 cccgagctgtggagcctcgcgaagacgcgtccgcagctgaactaagacagctgagccgc 1337
 DB 4692 CCCGCTGTGGGCTCCGCGCAAGAACCGGACATGAGTACGAGACATGGCGAGGG 4751
 QY 1338 ccatccgcaglatatcaagaaggacatccgcgaagccagacatcccgagcctc 1397
 DB 4752 CGCTGAGGTACTACTACAGCGCGGCGCATCTGCGCAAGTGGA---TGCCAGCGGCTGG 4808
 QY 1398 ttcaccagttcgtgca 1413
 DB 4809 TCATCAGATTCTGTGA 4824

RESULT 10
 DROE74B DROE74B 5315 bp mRNA INV 26-APR-1993
 LOCUS Drosophila melanogaster E74B protein.
 DEFINITION M37083.1 GI:157309
 ACCESSION
 VERSION
 KEYWORDS E74B protein.
 SOURCE D.melanogaster (strain Canton S), cDNA to mRNA, and DNA.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 5315)
 AUTHORS Butts,K.C., Thummel,C.S., Jones,C.W., Karim,F.D. and Hogness,D.S.

COMMENT
Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 1999 this sequence version replaced g1:5870264.

	NOTE: This is a 'working draft' sequence. It currently		
*	consists of 69 contigs. The true order of the pieces		
*	is not known and their order in this sequence record is		
*	arbitrary. Gaps between the contigs are represented as		
*	runs of N. But the exact sizes of the gaps are unknown.		
*	This record will be updated with the finished sequence		
*	as soon as it is available and the accession number will		
*	be preserved.		
*	1	1361:	contig of 1361 bp in length
*	1362	2336:	contig of 965 bp in length
*	2327	3249:	contig of 923 bp in length
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*	4027	5145:	contig of 1119 bp in length
*	5146	6228:	contig of 1083 bp in length
*	6329	6599:	contig of 761 bp in length
*	6590	8247:	contig of 1258 bp in length
*	8248	9676:	contig of 1429 bp in length
*	9677	11180:	contig of 1504 bp in length
*	11181	12034:	contig of 854 bp in length
*	12035	13512:	contig of 1478 bp in length
*	13513	14421:	contig of 909 bp in length
*	14422	15405:	contig of 984 bp in length
*	15406	16440:	contig of 1235 bp in length
*	16441	17488:	contig of 848 bp in length
*	17489	18402:	contig of 914 bp in length
*	18403	19172:	contig of 770 bp in length
*	19173	20126:	contig of 1144 bp in length
*	20317	21121:	contig of 805 bp in length
*	21122	22466:	contig of 1345 bp in length
*	22467	23838:	contig of 1372 bp in length
*	23839	25887:	contig of 2049 bp in length
*	25888	27457:	contig of 1570 bp in length
*	27458	28400:	contig of 943 bp in length
*	28401	29307:	contig of 907 bp in length
*	29308	31428:	contig of 2121 bp in length
*	31429	33032:	contig of 1604 bp in length
*	33033	34331:	contig of 1199 bp in length
*	34332	35530:	contig of 1299 bp in length
*	35531	37088:	contig of 1558 bp in length
*	37089	37921:	contig of 833 bp in length
*	37922	39529:	contig of 1608 bp in length
*	39530	40684:	contig of 1155 bp in length
*	40685	41916:	contig of 1232 bp in length
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*	42752	43564:	contig of 813 bp in length
*	43565	45392:	contig of 1828 bp in length
*	45393	47512:	contig of 2120 bp in length
*	47513	48967:	contig of 1455 bp in length
*	48968	50523:	contig of 1556 bp in length
*	50524	52009:	contig of 1486 bp in length
*	52010	53087:	contig of 1078 bp in length
*	53088	54948:	contig of 1861 bp in length
*	54949	56618:	contig of 1940 bp in length
*	56619	58561:	contig of 1673 bp in length
*	58562	59817:	contig of 1256 bp in length
*	59818	62089:	contig of 2272 bp in length
*	62090	64123:	contig of 2034 bp in length
*	64124	65968:	contig of 1845 bp in length
*	65969	68391:	contig of 2423 bp in length
*	68392	70326:	contig of 1937 bp in length
*	70329	72164:	contig of 2836 bp in length
*	72165	74288:	contig of 1124 bp in length
*	74289	76088:	contig of 1800 bp in length
*	76089	77229:	contig of 1141 bp in length
*	77230	80291:	contig of 3062 bp in length
*	80292	82144:	contig of 1853 bp in length
*	82145	84112:	contig of 1981 bp in length
*	84126	86442:	contig of 2317 bp in length
*	86443	88891:	contig of 2448 bp in length
*	88892	91665:	contig of 2774 bp in length
*	91666	94033:	contig of 2370 bp in length
*	94036	96551:	contig of 2516 bp in length
*	96552	99933:	contig of 3383 bp in length

REFERENCE 1 (bases 1 to 2266)
 AUTHORS Rao, V.N., Huebner, K., Isobe, M., ar-Rushdi, A., Croce, C.M. and Reddy, E.S.
 TITLE elk tissue-specific ets-related genes on chromosomes X and 14 near translocation breakpoints
 JOURNAL Science 244 (4500), 66-70 (1989)
 MEDLINE 89203250
 COMMENT On Sep 15, 1994 this sequence version replaced g1:341319.
 FEATURES location/Qualifiers
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 /cell_line="COLO 320"
 /clone="lambda-11"
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 /product="tyrosine kinase"
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 FTTLISIQPPPPHPPAVLPNAPAGAAAPSGSRSPSPLEACEAEAGAPLO
 VITTPPEANLSEELNVEPGIGALPPRYKREKRELEAVAGEFPEITKAPEV
 PPOECVPAFLPAYVMDTACAGAGHAASSEISOPKGRPRDLEPLSPSLGSGPPE
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 BASE COUNT 457 a 731 c 605 g 473 t
 ORIGIN

Query Match 4.68; Score 86.4; DB 9; Length 2266;
 Best Local Similarity 60.58; Pred. No. 2.3e-06;
 Matches 179; Conservative 0; Mismatches 111; Indels 6; Gaps 2;

QY 1166 ctgtgcaagttctcaagattgtctactcaagcccaagcctatgctcattatg 1225
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 DB 334 CTGTGCAAGTTTCTGCTGCAAGCTGCTGAGAGAG---CAAGGCAATGCGCAATCATCTCC 390
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 QY 1226 tggctcaagaagaaggacatctcaaatgaggactcagcccaagtgccgcgctg 1285
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 DB 391 TGGACTTCAAGCGATGCTGTAATTCAGCTGTGATGATGAGAGAGAGTGGCGCTG 450
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 QY 1286 tggggatcgcgaagaacgcgtccgcacatgaactacgacaaagctgagccgtccatcgc 1345
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 DB 451 TGGGGACTAGCGCAAGCAAGCAACATGAATTACGACAACTCAGCGGCGCTTGGCG 510
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 QY 1346 cagattataaagaaggacatcctcgaagcagacatcctcgaagcctctctacacg 1405
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 DB 511 TACTACTATGACAAAGAACTCATCCCAAG---GTGAGCGGCGCAGAAAGTTGCTACAAAG 567
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 QY 1406 ttcgtgcaccccatctgagtgctcgtgcccgaagcctgaaacccgcctcagaagcgc 1461
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 DB 568 TTTGTGTCTTACTACCTGAGGTGCGAGGCTCTCCACTGAGAGACTGCGCCGCCCAAGCC 623
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RESULT 15
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 LOCUS DEFINITION Gallus gallus ets domain protein (ERM) mRNA, partial cds.
 AF075706
 VERSION AF075706.1 GI:3869357
 KEYWORDS chicken.
 SOURCE Gallus gallus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauromia;
 Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 848)
 AUTHORS Lin, J.H., Salto, T., Anderson, D.J., Lance-Jones, C., Jessell, T.M. and Arber, S.
 TITLE Functionally related motor neuron pool and muscle sensory afferent subtypes defined by coordinate Ets gene expression
 JOURNAL Cell 95 (3), 393-407 (1998)
 MEDLINE 99029846
 REFERENCE 2 (bases 1 to 848)
 AUTHORS Lin, J.H., Salto, T., Anderson, D.J., Lance-Jones, C., Jessell, T.M. and Arber, S.
 TITLE Direct Submission
 JOURNAL Submitted (01-JUN-1998) Center for Neurobiology & Behavior, Columbia University, 701 W. 168th St. HNSC 1013, New York, NY 10032, USA
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 MOKVAGERVYKFEVCDPDAFLFMAVYPNORPFLKAEPDCHVSEEDTLPLHFFDSPAY
 LLEVEHCGSLPYAGFAV"
 BASE COUNT 192 a 265 c 245 g 146 t
 ORIGIN

Query Match 4.58; Score 84.8; DB 4; Length 848;
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 Matches 141; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

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Search completed: March 10, 2000, 18:55:42
 Job time: 4704 sec

GenCore version 4.5
 Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2000, 17:37:18 ; Search time 904.17 seconds

(without alignments)
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 Perfect score: 1894
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 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 362)
 AUTHORS Chen, T., Buntling, M., Karim, F.D. and Thummel, C.S.
 TITLE Isolation and characterization of five Drosophila genes that encode
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 JOURNAL Dev. Biol. 151, 176-191 (1992)
 MEDLINE 92249640
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 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 139371)
 AUTHORS Celniker, S.E., Agbayani, A., Arcalini, T.T., Baxter, E., Blazej, R.G.,
 Buttenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
 Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
 Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karris, K., Kearney, L.,
 Kim, E., Lee, B., Lewis, S., Li, P., Lomocan, M.A., Mazda, P.,
 Moshrefi, A.R., Moshrefi, M., Nixon, K., Paele, J.M., Park, S.,
 Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
 Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
 Rubin, G.M.
 TITLE Sequencing of Drosophila melanogaster
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 139371)
 AUTHORS Celniker, S.E., Agbayani, A., Arcalini, T.T., Baxter, E., Blazej, R.G.,
 Buttenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
 Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
 Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karris, K., Kearney, L.,
 Kim, E., Lee, B., Lewis, S., Li, P., Lomocan, M.A., Mazda, P.,
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 Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
 Rubin, G.M.
 COMMENT Submitted (30-JUL-1999) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA
 On Sep 24, 1999 this sequence version replaced gi:5902266.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive web site (<http://www.fruitfly.org/sequence/>) or send email
 to bdg@fruitfly.berkeley.edu. All contigs in this submission meet
 the following cutoffs: length >= 200 bases.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 82 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
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fruit fly.
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Drosophila melanogaster
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 137899)
Celiker,S.E., Aghayani,A., Arcaina,T.T., Baxter,E., Blazek,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K.,
Keatney,L., Lee,B., Lewis,S., Li,P., Lomocan,M.A., Mazda,P.,
Moshnefti,A.R., Moshnefti,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B.,
Richardson,S., Sethi,H., Sylvestre,R.R., Wan,K.H., Webster,D.,
Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.
TITLE
JOURNAL
REFERENCE
AUTHORS
Unpublished
2 (bases 1 to 137899)
Celiker,S.E., Aghayani,A., Arcaina,T.T., Baxter,E., Blazek,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
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Pfeiffer,B., Poon,L., Sequelstra,A., Sethi,H., Snir,E.,
Sylvestre,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
Rubin,G.M.
TITLE
JOURNAL
COMMENT
Submitted (14-JUN-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Nov 16, 1999 this sequence version replaced gi:5670465.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive web site (<http://www.fruitfly.org/sequence/>) or send email
to bdgs@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 81 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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10803 11555: contig of 753 bp in length
11556 11635: gap of unknown length
11636 12241: contig of 606 bp in length
12242 12321: gap of unknown length
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13550 14845: contig of 1296 bp in length
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14926 16090: contig of 1165 bp in length
16091 16170: gap of unknown length
16171 17409: contig of 1239 bp in length
17410 17489: gap of unknown length
17490 18567: contig of 1078 bp in length
18568 18647: gap of unknown length
18648 20255: contig of 1608 bp in length
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20336 22111: contig of 1776 bp in length
22112 22191: gap of unknown length
22192 23746: contig of 1555 bp in length
23747 23826: gap of unknown length
23827 25242: contig of 1416 bp in length
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27340 29015: gap of unknown length
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31255 31334: gap of unknown length
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34452 36983: contig of 2532 bp in length
36984 37063: gap of unknown length
37064 38444: contig of 1381 bp in length
38445 38524: gap of unknown length
38525 40637: contig of 2113 bp in length
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40718 42339: contig of 1632 bp in length
42340 44343: gap of unknown length
44341 44423: contig of 1924 bp in length
44424 46038: gap of unknown length
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47763 50292: contig of 2530 bp in length
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52287 52366: gap of unknown length
52367 53838: contig of 1472 bp in length
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65965	68395:	contig of 2431 bp in length
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74038	74117:	gap of unknown length
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81442	81521:	gap of unknown length
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85044	85123:	gap of unknown length
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88178	89257:	gap of unknown length
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97506	97585:	gap of unknown length
97586	102127:	contig of 4542 bp in length
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102208	106803:	contig of 4596 bp in length
106804	106883:	gap of unknown length
106884	111766:	contig of 4883 bp in length
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111847	120329:	contig of 8483 bp in length
120330	120409:	gap of unknown length
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121195	121274:	gap of unknown length
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121914	122655:	contig of 652 bp in length
122656	122645:	gap of unknown length
122646	123349:	contig of 704 bp in length
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123430	124228:	contig of 799 bp in length
124229	124308:	gap of unknown length
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125778	125857:	gap of unknown length
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126519	127146:	contig of 628 bp in length
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127227	127823:	contig of 597 bp in length
127824	127903:	gap of unknown length
127904	128353:	contig of 450 bp in length
128354	128433:	gap of unknown length
128434	129048:	contig of 615 bp in length
129049	129128:	gap of unknown length
129129	129830:	contig of 702 bp in length
129831	129910:	gap of unknown length
129911	130533:	contig of 623 bp in length
130534	130613:	gap of unknown length
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Db 114230 GCCAAGCTGTGGGGTTCGGCCGCMAAACCGACCGCGGTGAACATATGATTAAGTTGTCCCGC 114171

QY 1337 tccatccgcagatattacaagaagggcatatccggaagcagacacatctccagcgcctc 1396

Db 114170 TCCATCCAGCGAGTACTCAAGAAAAGGAATCATGAAAAAGACGGAGAGGTCAACGGCGGTC 114111

QY 1397 gtctacagattgcgcaccccatctg 1422

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DEFINITION	AC008217 121935 bp DNA HTG 02-AUG-1999	
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	10.9.3 map 98B-98B strain Y; cn bw sp, *** SEQUENCING IN PROGRESS	
	***, 94 unordered pieces.	
ACCESSION	AC008217	
VERSION	AC008217.2	GI:5670464
KEYWORDS	HTG; HTGS_PHASE1.	
SOURCE	fruit fly.	

ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridiidae; Drosophilidae; Drosophila.
1 (bases 1 to 121935)
REFERENCE
AUTHORS
Celisner, S.E., Agbayan, A., Arcaina, T.T., Baxter, E., Blazet, R.

TITLE	JOURNAL	REFERENCE	AUTHORS
Unpublished		2 (bases 1 to 121935)	Celnikier, S. E., Aghayani, A., Arcalaina, T. T., Baxter, E., Blazek, R. G.
Butenhoff, C., Champe, M., Chavez, C., Chev, M., Ciesiolka, L., Doyle, C. M., Farfan, D. E., Galle, R., George, R. A., Harris, N. L., Hoskins, R. A., Houston, K. A., Hummstedt, S. R., Katra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomoth, M. A., Mazda, P., Moshell, A. R., Moshell, M., Nixon, K., Pacible, J. M., Park, S., Pfeiffer, B., Poon, L., Sequelieri, A., Setli, H., Shi, E., Svitskas, R. R., Wan, K. H., Weinburg, T., Zhang, R., Zieran, L. L. and Rubin, G. M.			
Rebinding of <i>Drosophila melanogaster</i>			

TITLE Direct Substitution
JOURNAL Submitted (23-JUL-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT On Aug 2, 1999 this sequence version replaced q1:5649213.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (<http://www.fruitfly.org/sequence/>) or send email to bdg@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

- * NOTE: This is a 'working draft' sequence. It currently consists of 94 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
- * This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
* 1 846: contig of 846 bp in length
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* 1710 2954: contig of 1245 bp in length
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* 96543 96622: gap of unknown length
* 96623 97226: contig of 604 bp in length
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* 103790 104473: gap of unknown length
* 104474 104553: contig of 684 bp in length
* 104554 105266: gap of unknown length
* 105267 105346: contig of 713 bp in length
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DB 391 tggacttcacggcgatgtgtgaattcaaggctgtgagacagagagtgccggctg 450
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OY 1286 tgggacatccgagaagaacgctccgcatgtaactagcaagaactgaagccgctccatcgc 1345
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OY 1346 cagtatcaagaagaagagcattccggaagccagacatctccagcgctgtccacag 1405
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OY 1406 ttctgaccccccatctgagtgctgcccagggcctgaaccgcccctcaaggagcc 1461
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RESULT 15
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ACCESSION AF075706
VERSION AF075706.1 GI:3869357
KEYWORDS
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 848)
Lin.J.H., Saito,T., Anderson,D.J., Lance-Jones,C., Jessell,T.M. and
Arber,S.
FUNCTIONALLY related motor neuron pool and muscle sensory afferent
subtypes defined by coordinate ERS gene expression
Cell 95 (3), 393-407 (1998)
99029846
2 (bases 1 to 848)
Lin.J.H., Saito,T., Anderson,D.J., Lance-Jones,C., Jessell,T.M. and
Arber,S.
Direct Submission
Submitted (01-JUL-1998) Center for Neurobiology & Behavior,
Columbia University, 701 W. 168th St. HNSC 1013, New York, NY
10032, USA

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DB 365 ttcaagctgactgagaccgagagaggtagcagcgcttgccatccagagacggccg 424
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OY 1310 gccatgaactcagcaagctgagccgtctcactccgacagatltcaagaagagcattc 1369
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DB 425 gccatgaactcagcaagctgagccgtctcactccgacagatltcaagaagagcattc 484
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OY 1370 cggagccagacatctccagcgctcgtctcaacagttcgtgacacccatctgagtcct 1429
|||||
DB 485 cagaaag---gtggccggcgagcggctgactcttcaagattgtgtgaccccgagccctc 541
|||||
OY 1430 ggcacagggcctgaagaccgcccctcaaggagccttc 1465
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DB 542 ttcttcacatgggtgtaaccggaacatcagggcccttc 577
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Job time: 4704 sec